



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: EVANS, RONALD M.  
MCKEOWN, MICHAEL B.  
ORO, ANTHONY E.  
SEGRAVES, WILLIAM A.  
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(ii) TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE  
STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE  
ULTRASPIRACLE RECEPTOR

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/907,908  
(B) FILING DATE: 02-JUL-1992  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 31192  
(C) REFERENCE/DOCKET NUMBER: P41 9321

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 163..1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACACGGTG GCGTTGCCAA AGTGAACCC CAACAGAGAG GCGAAAGCGA GCCAAGACAC

60

ACCACATACA CACGAAGAGA ACGAGCAAGA AGAAACCGGT AGGCAGGAGGA GGCGCTGCC

120

CCAGTTCCCTC CAATATAACCC AGCACCAACAT CACAAGCCCCA GG ATG GAC AAC TGC Met Asp Asn Cys 1	174
GAC CAG GAC GCC AGC TTT CGG CTG AGC CAC ATC AAG GAG GAG GTC AAG Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys Glu Glu Val Lys 5 10 15 20	222
CCG GAC ATC TCG CAG CTG AAC GAC AGC AAC AAC AGC AGG TTT TCG CCC Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser Ser Phe Ser Pro 25 30 35	270
AAG GCC GAG AGT CCC GTG CCC TTC ATG CAG GCC ATG TCC ATG GTC CAC Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met Ser Met Val His 40 45 50	318
GTG CTG CCC GGC TCC AAC TCC GCC AGC TCC AAC AAC AAC AGC GCT GGA Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn Asn Ser Ala Gly 55 60 65	366
GAT GCC CAA ATG GCG CAG GCG CCC AAT TCG GCT GGA GGC TCT GCC GCC Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly Gly Ser Ala Ala 70 75 80	414
GCT GCA GTC CAG CAG TAT CCG CCT AAC CAT CCG CTG AGC GGC AGC Ala Ala Val Gln Gln Tyr Pro Pro Asn His Pro Leu Ser Gly Ser 85 90 95 100	462
AAG CAC CTC TGC TCT ATT TGC GGG GAT CGG GCC AGT GGC AAG CAC TAC Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr 105 110 115	510
GGC GTG TAC AGC TGT GAG GGC TGC AAG GGC TTC TTT AAA CGC ACA GTG Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val 120 125 130	558
CGC AAG GAT CTC ACA TAC GCT TGC AGG GAG AAC CGC AAC TGC ATC ATA Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg Asn Cys Ile Ile 135 140 145	606
GAC AAG CGG CAG AGG AAC CGC TGC CAG TAC TGC CGC TAC CAG AAG TGC Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys 150 155 160	654
CTA ACC TGC GGC ATG AAG CGC GAA GCG GTC CAG GAG GAG CGT CAA CGC Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg 165 170 175 180	702
GGC GCC CGC AAT GCG GCG GGT AGG CTC AGC GCC AGC GGA GGC GGC AGT Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser Gly Gly Ser 185 190 195	750
AGC GGT CCA GGT TCG GTA GGC GGA TCC AGC TCT CAA GGC GGA GGA GGA Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln Gly Gly Gly 200 205 210	798
GGA GGC GGC GTT TCT GGC GGA ATG GGC AGC GGC AAC GGT TCT GAT GAC Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn Gly Ser Asp Asp 215 220 225	846
TTC ATG ACC AAT AGC GTG TCC AGG GAT TTC TCG ATC GAG CGC ATC ATA Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile Glu Arg Ile Ile 230 235 240	894
GAG GCC GAG CAG CGA GCG GAG ACC CAA TGC GGC GAT CGT GCA CTG ACG Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp Arg Ala Leu Thr 245 250 255 260	942

TTC CTG CGC GTT GGT CCC TAT TCC ACA GTC CAG CCG GAC TAC AAG GGT Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro Asp Tyr Lys Gly 265 270 275	990
GCC GTG TCG GCC CTG TGC CAA GTG GTC AAC AAA CAG CTC TTC CAG ATG Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln Leu Phe Gln Met 280 285 290	1038
GTC GAA TAC GCG CGC ATG ATG CCG CAC TTT GCC CAG GTG CCG CTG GAC Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln Val Pro Leu Asp 295 300 305	1086
GAC CAG GTG ATT CTG CTG AAA GCC GCT TGG ATC GAG CTG CTC ATT GCG Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu Leu Leu Ile Ala 310 315 320	1134
AAC GTG GCC TGG TGC AGC ATC GTT TCG CTG GAT GAC GGC GGT GCC GGC Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp Gly Gly Ala Gly 325 330 335 340	1182
GGC GGG GGC GGT GGA CTA GGC CAC GAT GGC TCC TTT GAG CGA CGA TCA Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe Glu Arg Arg Ser 345 350 355	1230
CCG GGC CTT CAG CCC CAG CAG CTG TTC CTC AAC CAG AGC TTC TCG TAC Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln Ser Phe Ser Tyr 360 365 370	1278
CAT CGC AAC AGT GCG ATC AAA GCC GGT GTG TCA GCC ATC TTC GAC CGC His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala Ile Phe Asp Arg 375 380 385	1326
ATA TTG TCG GAG CTG AGT GTA AAG ATG AAG CGG CTG AAT CTC GAC CGA Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu Asn Leu Asp Arg 390 395 400	1374
CGC GAG CTG TCC TGC TTG AAG GCC ATC ATA CTG TAC AAC CCG GAC ATA Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr Asn Pro Asp Ile 405 410 415 420	1422
CGC GGG ATC AAG AGC CGG GCG GAG ATC GAG ATG TGC CGC GAG AAG GTG Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys Arg Glu Lys Val 425 430 435	1470
TAC GCT TGC CTG GAC GAG CAC TGC CGC CTG GAA CAT CCG GGC GAC GAT Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His Pro Gly Asp Asp 440 445 450	1518
GGA CGC TTT GCG CAA CTG CTG CGT CTG CGC CGC TTT GCG ATC GAT Gly Arg Phe Ala Gln Leu Leu Arg Leu Arg Arg Phe Ala Ile Asp 455 460 465	1566
CAG CCT GAA GTG CCA GGA TCA CCT GTT CCT CTT CCG CAT TAC CAG CGA Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro His Tyr Gln Arg 470 475 480	1614
CCG GCC GCT GGA GGA GCT CTT TCT CGA GCA GCT GGA GGC GCC GCC Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly Gly Ala Ala Ala 485 490 495 500	1662
ACC CGG CCT GGC GAT GAA ACT GGA GTA GGG TCC CGA CTC TAAAGTCGCC Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg Leu 505 510	1711
CCCGTTCTCC ATCCGAAAAA TGTTTCATTG TGATTGCGTT TGTTGCATT TCTCCTCTCT	1771
ATCCCTACAA AAGCCCCCTA ATATTACGCA AAATGTGTAT GTAATTGTTT ATTTTTTTT	1831

TATTACCTAA TATTATTATT ATTATTGATA TAGAAAATGT TTTCCTTAAG ATGAAGATTA	1891
GCCTCCTCGA CGTTTATGTC CCAGTAAACG AAAAACAAAC AAAATCCAAA ACTTGAAAAG	1951
AACACAAAC ACGAACGAGA AAATGCACAC AAGCAAAGTA AAAGTAAAAG TTAAACTAAA	2011
GCTAAACGAG TAAAGATATT AAAATAACGG TTAAAATTAA TGCATAGTTA TGATCTACAG	2071
ACGTATGTAA ACATACAAAT TCAGCATAAA TATATATGTC AGCAGGGCA TATCTCGGT	2131
GCTGGCCCCG TTCTAAACCA ATTGTAATTA CTTTTAACCA TAAATTACC CAAAACGTTA	2191
TCAATTAGAT GCGAGATACA AAAATCACCG ACGAAAACCA ACAAAATATA TCTATGTATA	2251
AAAAATATAA GCTGCATAAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	2304

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys  
 1                   5                   10                   15

Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser  
 20               25                   30

Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met  
 35               40                   45

Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn  
 50               55                   60

Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly  
 65               70                   75                   80

Gly Ser Ala Ala Ala Val Gln Gln Tyr Pro Pro Asn His Pro  
 85               90                   95

Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser  
 100              105                   110

Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe  
 115              120                   125

Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg  
 130              135                   140

Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg  
 145              150                   155                   160

Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu  
 165              170                   175

Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser  
 180              185                   190

Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln  
 195              200                   205

Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn  
 210 215 220  
 Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile  
 225 230 235 240  
 Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp  
 245 250 255  
 Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro  
 260 265 270  
 Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln  
 275 280 285  
 Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln  
 290 295 300  
 Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu  
 305 310 315 320  
 Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp  
 325 330 335  
 Gly Gly Ala Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe  
 340 345 350  
 Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln  
 355 360 365  
 Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala  
 370 375 380  
 Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu  
 385 390 395 400  
 Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr  
 405 410 415  
 Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys  
 420 425 430  
 Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His  
 435 440 445  
 Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Arg Leu Arg Arg  
 450 455 460  
 Phe Ala Ile Asp Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro  
 465 470 475 480  
 His Tyr Gln Arg Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly  
 485 490 495  
 Gly Ala Ala Ala Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg  
 500 505 510  
 Leu

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Asp	Xaa	Ala	Xaa	Gly	Xaa	Tyr	Xaa	Xaa	Xaa
1															15
Xaa	Cys	Xaa	Xaa	Cys	Lys	Xaa	Phe	Phe	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	
					20										30
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys							
						35									45
Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Arg	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Arg	Xaa	Xaa
			50			55									60
Lys	Cys	Xaa	Xaa	Xaa	Gly	Met									
			65			70									

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGTCAAGGA	GGTCA	15
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## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGAATGA	GGACAA	15
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## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGAAACGG GGGCA

15

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCACGAG GTTCA

15

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGTTCACAGG AGGTCA

16

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGTGACAGG AGGTCA

16

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGTGACAGG AGGACA

16

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGTTAGGGG AGGACA

16

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCATTTC AGGTCC

16

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGTCACCAG GAGGTCA

17

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGGTGAACAG GAGGTCA

17

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTCACCGA AAGTTCA

17

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCACCGA AAGTTCA

17

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCACTGA CAGGGCA

17

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGTCATTCA GAGTTCA

17

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAGCTTAAGG GTTCACCGAA AGTTCACTCA GCTT

34

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATAGCTT

38

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATATATTAG CTT

43

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTCGATGG ACAAGTGCAT TGAACCCTTG AGCTACCTGT TCACGTAACT TGGGAACTTC	60
GA	62

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTGCGCCAC GGCGGCCGCC GGAGCTGTGC CTG	33
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## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGGGTATGC GCCTCGAGTG CGTCGTCCC	29
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## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGGACAAAGG TCA	13
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## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGACAAG TGCATTGAAC CCTTGTCCTCT

30

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCTGTGCA TTGAACGTGC TCGA

24

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGAAGTGCA TTGAACCCGC TCGA

24

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAAGGATCT TGACCCCAAT GAACTTCTTA

30